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Amendments to the Specification:

Please delete the previously filed Sequence Listing and insert the substitute Sequence Listing filed herewith.

Please amend the specification as follows:

Please amend paragraph [0011] of the above-identified application, or paragraph [0015] of the published application (20030157695) with the following amended paragraph.

[0011] 4. Comparison with a deposit of a type strain at the ATCC (American Type Culture Collection; 12301 Parklawn Drive; Rockville, Md. 20852) on Sep. 27, 2000 under number ATCC PTA-2501.

Please amend paragraph [0026] of the above-identified application, or paragraph [0030] of the published application (20030157695) with the following amended paragraph. Please note that paragraph [0026] was previously twice amended: 1) response to the Office Action dated February 15, 2005; and 2) response to the Office Action dated September 15, 2003. The following amendment incorporates all previous amendments to paragraph [0026].

[0026] The Salinospora group was initially recognized after phylogenetic characterization of sediment-derived actinomycetes isolated during an expedition to the Bahamas. Partial 16S rDNA gene sequences from eight morphologically diverse strains indicated the presence of four signature nucleotides between positions 198 to 1424 of SEQ ID NOs: 3, 4 and 5, or nucleotide positions 207-468 (based on the *E. coli* 16S rRNA numbering system which is well known to those skilled in the art; see also Table 3 which utilizes the *E. coli* 16S rRNA numbering system in comparing the Salinospora actinomycetes of the present invention to those of other Micromonosporaceae genera). These signatures nucleotides have subsequently been found in all 45 partially sequenced Salinospora strains. Two strains showing the highest phylogenetic diversity (CNH643 and CNH646) were sequenced nearly in their entirety (GenBank accession numbers AY040619 (SEQ ID NO:3) and AY040620 (SEQ

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ID NO:4), respectively) and found to possess one additional signature nucleotide (position 1456) that is also characteristic of this group (Table 3). Phylogenetic analyses of aligned sequences from these strains indicate that they form a distinct and coherent clade within the *Micromonosporaceae* (Figure 2). Signature nucleotides unify this clade and a high bootstrap value supports clear separation from the nine currently described genera within the family. <u>SEQ ID NOs: 3 and 4 are identical sequences. SEQ ID NO:4 is derived from strain CNH646</u>, which was deposited September 27, 2000 (ATCC No. PTA-2501).

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Please amend paragraph [0028] of the above-identified application, or paragraph [0032] of the published application (20030157695) with the following amended paragraph. Please note that paragraph [0028] was previously amended in the response to the Office Action dated September 15, 2003. The following amendment incorporates all previous amendments to paragraph [0028].

[0028] A follow-up study was undertaken in the Bahamas to determine the persistence of the *Salinospora* group. From 20 samples collected from four transects (0-30 m), 355 actinomycetes were observed and over 90% of these displayed characteristic *Salinospora* morphologies suggesting that this group may be the numerically dominant actinomycete in marine sediments. Of those observed, 100 strains were isolated for further study. The average numbers of *Salinospora* colony-forming units (cfu's) ranged from 1.2-2.3 x 10³ cfu's/ml sediment. Over 50% of the *Salinospora* isolates appeared on a low nutrient medium (M4) indicating the importance of using appropriate isolation techniques. Thirteen representatives of eight different colony morphotypes were partially sequenced and the most phylogenetically diverse isolate (CNH898) was sequenced nearly in its entirety (GenBank Accession number AY040622) (SEQ ID NO:5). Strain CNH898 was deposited June 30, 2003 (ATCC No. PTA-5275).

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Please amend paragraph [0032] of the above-identified application, or paragraph [0036] of the published application (20030157695) with the following amended paragraph. Please note that paragraph [0032] was previously amended in the response to the Office Action dated September 15, 2003. The following amendment incorporates all previous amendments to paragraph [0032].

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[0032] To determine if *Salinospora* members had a broader distribution, sediments were collected from the Red Sea and the Sea of Cortez. From 42 Red Sea sediment samples, 22 isolates with *Salinospora* morphologies and an obligate requirement of seawater for growth were obtained. Six isolates representing 4 major morphotypes were partially sequenced and the almost complete 16S rDNA sequence of one strain (CNH725, GenBank Accession number AY040621)-(SEQ ID NO:8) is represented in Figure 3. From 36 sediments collected in the Sea of Cortez, 20 seawater-requiring actinomycete strains were isolated and all of these possessed *Salinospora* morphological characteristics. Eight strains representing five different morphotypes were partially sequenced and the phylogenetically diverse isolate CNH964 (GenBank Accession number <u>AY040623 (SEQ ID NO:9)</u>) was sequenced almost in its entirety. These results clearly indicate that *Salinospora* members are widely distributed in marine sediments.

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Please amend Table 3 of the above-identified application with the following amended Table 3. Please note that paragraph Table 3 was previously amended in the response to the Office Action dated February 15, 2005. The following amendment incorporates all previous amendments to Table 3.

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Table 3.

Relative Nucleotide	All Other	Salinospora	Nucleotide Positions
Position of <i>E.coli</i> 16S	Micromonosporaceae	Isolates	of SEQ ID NOs: [[3*,
rRNA	Genera		4, and 5]] <u>4 and 5</u>
207	(U/C)	A	198
366	(A/G)	С	351
467	(A/G)	U	442 or 443*
468	A	U	443 or 444*
1456	A	G	1423 or 1424*

Sequence Listing

An amended Sequence Listing is also enclosed. Following the abstract, please insert the attached Sequence Listing with subsequent page numbering thereafter.